



SEQUENCE LISTING

<110> Ambion, Inc.
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Setterquist, Robert
Latham, Gary

<120> Recombinant Reverse Transcriptases

<130> AMBI:1001

<140> 10/827,498

<141> 2004-01-19

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<170> PatentIn version 3.3

<210> 1

<211> 2037

<212> DNA

<213> Moloney murine sarcoma virus

<220>

<221> CDS

<222> (1)..(2037)

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Glu	Pro	Asp	Val	Ser	Leu	Gly	Ser	Thr	Trp	Leu	Ser	Asp	Phe	Pro	Gln	
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gcc	tgg	gcg	gaa	acc	ggg	ggc	atg	gga	ctg	gca	gtt	cgc	caa	gct	cct	144
Ala	Trp	Ala	Glu	Thr	Gly	Gly	Met	Gly	Leu	Ala	Val	Arg	Gln	Ala	Pro	
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ctg	atc	ata	cct	ctg	aaa	gca	acc	tct	acc	ccc	gtg	tcc	ata	aaa	caa	192
Leu	Ile	Ile	Pro	Leu	Lys	Ala	Thr	Ser	Thr	Pro	Val	Ser	Ile	Lys	Gln	
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tac	ccc	atg	tca	caa	gaa	gcc	aga	ctg	ggg	atc	aag	ccc	cac	ata	cag	240
Tyr	Pro	Met	Ser	Gln	Glu	Ala	Arg	Leu	Gly	Ile	Lys	Pro	His	Ile	Gln	
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aga	ctg	ttg	gac	cag	gga	ata	ctg	gta	ccc	tgc	cag	tcc	ccc	tgg	aac	288
Arg	Leu	Leu	Asp	Gln	Gly	Ile	Leu	Val	Pro	Cys	Gln	Ser	Pro	Trp	Asn	
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acg	ccc	ctg	cta	ccc	gtt	aag	aaa	cca	ggg	act	aat	gat	tat	agg	cct	336
Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro	
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gtc	cag	gat	ctg	aga	gaa	gtc	aac	aag	cgg	gtg	gaa	gac	atc	cac	ccc	384
Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro	
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acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc cca ccg tcc cac Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His 130 135 140	432
cag tgg tac act gtg ctt gat tta aag gat gcc tat ttc tgc ctg aga Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Tyr Phe Cys Leu Arg 145 150 155 160	480
ctc cac ccc acc agt cag cct ctc ttc gcc ttt gag tgg aga gat cca Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro 165 170 175	528
gag atg gga atc tca gga caa ttg acc tgg acc aga ctc cca cag ggt Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly 180 185 190	576
ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cac aga gac cta Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu His Arg Asp Leu 195 200 205	624
gca gac ttc cgg atc cag cac cca gac ttg atc ctg cta cag tac gtg Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val 210 215 220	672
gat gac tta ctg ctg gcc gcc act tct gag cta gac tgc caa caa ggt Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly 225 230 235 240	720
act cgg gcc ctg tta caa acc cta ggg aac ctc ggg tat cgg gcc tcg Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly Tyr Arg Ala Ser 245 250 255	768
gcc aag aaa gcc caa att tgc cag aaa cag gtc aag tat ctg ggg tat Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr 260 265 270	816
ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr 275 280 285	864
gtg atg ggg cag cct act ccg aag acc cct cga caa cta agg gag ttc Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe 290 295 300	912
cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct ggg ttt gca gaa Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu 305 310 315 320	960
atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg act ctg ttt aat Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn 325 330 335	1008
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cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu 355 360 365	1104

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att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro 420 425 430	1296
cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro 435 440 445	1344
ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu 450 455 460	1392
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 Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
 610 615 620

ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt ccc ggg ggt caa 1920
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aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg 1968
 Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
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Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
 35 40 45

Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
 50 55 60

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
 65 70 75 80

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
 85 90 95

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
 100 105 110

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
 115 120 125

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
 130 135 140

Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Tyr Phe Cys Leu Arg
 145 150 155 160

Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
 165 170 175

Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
 180 185 190

Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu His Arg Asp Leu
 195 200 205

Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
 210 215 220

Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
 225 230 235 240

Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly Tyr Arg Ala Ser
 245 250 255

Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
 260 265 270

Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
 275 280 285

Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
 290 295 300

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
 305 310 315 320

Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
 325 330 335

Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
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Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
 355 360 365

Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
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Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
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Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
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Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
420 425 430

Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
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Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
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Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
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Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Asp Gly Ser Ser
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Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
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Lys Lys Leu Asn Val Tyr Thr Asp Ser Arg Tyr Ala Phe Ala Thr Ala
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His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu
595 600 605

Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
610 615 620

Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly Gly Gln
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Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
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